IN THE CLAIMS

Please amend the claims as follows. This listing of claims replaces all prior versions.

1. (Previously presented) A method of identifying a human subject having an increased sensitivity to warfarin, wherein a therapeutic dose of warfarin for the subject is lower than a therapeutic dose of warfarin for a normal subject, comprising detecting in the subject the presence of a single nucleotide polymorphism in the VKOR gene, wherein the single nucleotide polymorphism is correlated with increased sensitivity to warfarin, thereby identifying the subject having increased sensitivity to warfarin.

2. (Previously presented) The method of claim 1, wherein the subject is Caucasian and the single nucleotide polymorphism in the VKOR gene is a G→ C alteration at nucleotide 2581 of the nucleotide sequence of SEQ ID NO:11.

3. (Original) A method of identifying a human subject having increased sensitivity to warfarin, comprising:

a) correlating the presence of a single nucleotide polymorphism in the VKOR gene with increased sensitivity to warfarin; and

b) detecting the single nucleotide polymorphism of step (a) in the subject, thereby identifying a subject having increased sensitivity to warfarin.

4. (Previously presented) A method of identifying a single nucleotide polymorphism in the VKOR gene correlated with increased sensitivity to warfarin, comprising:

a) identifying a human subject having increased sensitivity to warfarin;

b) detecting in a population of the subjects of (a) above the presence of a single nucleotide polymorphism in the VKOR gene; and

c) correlating the presence of the single nucleotide polymorphism of step (b) with the increased sensitivity to warfarin in the population of subjects, thereby identifying a single nucleotide polymorphism in the VKOR gene correlated with increased sensitivity to

warfarin.

5. (Previously presented) A method of correlating a single nucleotide polymorphism in the VKOR gene of a human subject with increased sensitivity to warfarin, comprising:

a) identifying a subject having increased sensitivity to warfarin;

b) determining the nucleotide sequence of the VKOR gene in a population of the subjects of (a);

c) comparing the nucleotide sequence of step (b) with the wild type nucleotide sequence of the VKOR gene;

d) detecting a single nucleotide polymorphism in the nucleotide sequence of (b); and

e) correlating the single nucleotide polymorphism of (d) with increased sensitivity to warfarin in the subject of (a).

6-16. (Canceled).

17. (Previously presented) A method of screening for a single nucleotide polymorphism in the VKOR gene of a human subject that is associated with increased sensitivity to warfarin, comprising:

a) detecting single nucleotide polymorphisms in the VKOR gene of a human subject;

b) performing a population based study to detect the polymorphisms in a group of human subjects with increased sensitivity to warfarin and ethnically matched controls;

c) identifying an allele of a single nucleotide polymorphism in the VKOR gene that is associated with increased sensitivity to warfarin.

18. (New) A method of amplifying a segment of a VKOR genomic nucleotide sequence comprising:

a) choosing a first oligonucleotide primer from the 3′ end of the nucleotide sequence of SEQ ID NO:8;

b) choosing a second oligonucleotide primer from the 5′ end of the nucleotide sequence of SEQ ID NO:8;

c) adding said first primer and said second primer to a nucleic acid sample; and

d) amplifying a segment of the VKOR genomic nucleotide sequence defined by the first primer and the second primer.

19. (New) The method of claim 18, wherein the amplified segment of step (d) is less than 100 base pairs in length.

20. (New) The method of claim 18, wherein the amplified segment of step (d) comprises a single nucleotide polymorphism.

21. (New) The method of claim 18, wherein the amplified segment of step (d) comprises an allele of a single nucleotide polymorphism that is correlated with increased sensitivity to warfarin.

22. (New) The method of claim 18, wherein the nucleic acid sample is from a subject in need of warfarin therapy.

23. (New) The method of claim 18, wherein the first oligonucleotide primer is at least 15 nucleotides in length.

24. (New) The method of claim 18, wherein the second oligonucleotide primer is at least 15 nucleotides in length.

25. (New) A method of amplifying a segment of a VKOR genomic nucleotide sequence comprising:

a) choosing a first oligonucleotide primer from the nucleotide sequence of SEQ ID NO:8;

b) choosing a second oligonucleotide primer from the nucleotide sequence of SEQ ID NO:8 that differs in nucleotide sequence from the first oligonucleotide primer;

c) adding said first primer and said second primer to a nucleic acid sample; and

d) amplifying a segment of the VKOR genomic nucleotide sequence defined by the first primer and the second primer.

26. (New) The method of claim 25, wherein the amplified segment of step (d) is less than 100 base pairs in length.

27. (New) The method of claim 25, wherein the amplified segment of step (d) comprises a single nucleotide polymorphism.

28. (New) The method of claim 25, wherein the amplified segment of step (d) comprises an allele of a single nucleotide polymorphism that is correlated with increased sensitivity to warfarin.

29. (New) The method of claim 25, wherein the nucleic acid sample is from a subject in need of warfarin therapy.

30. (New) The method of claim 25, wherein the first oligonucleotide primer is at least 15 nucleotides in length.

31. (New) The method of claim 25, wherein the second oligonucleotide primer is at least 15 nucleotides in length.

32. (New) A method of amplifying a segment of a VKOR coding nucleotide sequence comprising:

a) choosing a first oligonucleotide primer from the 3′ end of the nucleotide sequence of SEQ ID NO:9;

b) choosing a second oligonucleotide primer from the 5′ end of the nucleotide sequence of SEQ ID NO:9;

c) adding said first primer and said second primer to a nucleic acid sample; and

d) amplifying a segment of the VKOR coding nucleotide sequence defined by the first primer and the second primer.

33. (New) The method of claim 32, wherein the amplified segment of step (d) is less than 100 base pairs in length.

34. (New) The method of claim 32, wherein the amplified segment of step (d) comprises a single nucleotide polymorphism.

35. (New) The method of claim 32, wherein the amplified segment of step (d) comprises an allele of a single nucleotide polymorphism that is correlated with increased sensitivity to warfarin.

36. (New) The method of claim 32, wherein the nucleic acid sample is from a subject in need of warfarin therapy.

37. (New) The method of claim 32, wherein the first oligonucleotide primer is at least 15 nucleotides in length.

38. (New) The method of claim 32, wherein the second oligonucleotide primer is at least 15 nucleotides in length.

39. (New) A method of amplifying a segment of a VKOR coding nucleotide sequence comprising:

a) choosing a first oligonucleotide primer from the nucleotide sequence of SEQ ID NO:9;

b) choosing a second oligonucleotide primer from the nucleotide sequence of SEQ ID NO:9 that differs in nucleotide sequence from the first oligonucleotide primer;

c) adding said first primer and said second primer to a nucleic acid sample; and

d) amplifying a segment of the VKOR coding nucleotide sequence defined by the first primer and the second primer.

40. (New) The method of claim 39, wherein the amplified segment of step (d) is less than 100 base pairs in length.

41. (New) The method of claim 39, wherein the amplified segment of step (d) comprises a single nucleotide polymorphism.

42. (New) The method of claim 39, wherein the amplified segment of step (d) comprises an allele of a single nucleotide polymorphism that is correlated with increased sensitivity to warfarin.

43. (New) The method of claim 39, wherein the nucleic acid sample is from a subject in need of warfarin therapy.

44. (New) The method of claim 39, wherein the first oligonucleotide primer is at least 15 nucleotides in length.

45. (New) The method of claim 39, wherein the second oligonucleotide primer is at least 15 nucleotides in length.